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EXAMINER	
THOMAS, DAVID C	
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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/731,419	BEJJANI ET AL.	
	Examiner	Art Unit	
	David C. Thomas	1637	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *25 May 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1,2,4,5,8,9,11,16,21-23,51-53,71,72 and 74-80* is/are pending in the application.

4a) Of the above claim(s) *51-53* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,2,4,5,8,9,11,16,21-23,71,72 and 74-80* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Continued Examination Under 37 CFR 1.114

1. A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on May 24, 2007 has been entered. Claims 1, 4, 5, 8, 9, 16, 71 and 74 (currently amended), claims 2, 11, 21-23 and 72 (original or previously presented) and claims 75-80 (newly added) will be examined on the merits. Claims 51-53 were previously withdrawn. Claims 7 and 73 are newly canceled and claims 3, 6, 10, 12-15, 17-20, 24-50 and 54-70 were previously canceled.

Claim Rejections - 35 USC § 102

2. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

3. Claims 71, 72 and 74 are rejected under 35 U.S.C. 102(a) as being anticipated by Gordon et al. (U.S. Patent No. 6,607,911).

With regard to claim 71, Gordon teaches a method, comprising:

designing multiple reference nucleic acids (separate constructs containing mutations such as deltaF508 and delta1507 in exons 10 and 11, respectively, in human

CFTR gene, column 3, lines 12-27 and column 16, lines 29-32), wherein each reference nucleic acid comprises an arrangement of bases emulating a clinically relevant site of a human nucleic acid exclusive of clinically irrelevant human nucleic acid adjacent to the clinically relevant site *in vivo* (fragments of control DNA construct used as reference standard may contain, for example, only exons and their intronic borders from cystic fibrosis transmembrane conductance regulator (CFTR) gene, each with associated mutant, column 16, lines 26-32);

synthesizing, base by base for each reference nucleic acid, a first mixture of various of the reference nucleic acids (fragment containing cassette for first reference site was amplified using unique priming sites, column 23, line 60 to column 24, line 3; fragment can also be made chemically or by other means, column 22, lines 30-37), wherein each of the various reference nucleic acids in the first mixture includes one or more tags allowing PCR amplification of the first mixture via a primer set specific to the tags of the first mixture (one or more primer sites for PCR were added to the cassette that also include unique restriction sites, column 23, lines 52-59); and

synthesizing, base by base for each reference nucleic acid, a second mixture of various of the reference nucleic acids (fragment containing cassette for second reference site was amplified using unique priming sites, column 23, line 60 to column 24, line 3; fragment can also be made chemically or by other means, column 22, lines 30-37), wherein each of the various reference nucleic acids in the second mixture includes one or more tags allowing PCR amplification of the second mixture via a second primer set specific to the tags of the second mixture (one or more primer sites

for PCR were added to the cassette that also include unique restriction sites, column 23, lines 52-59).

With regard to claim 72, Gordon teaches a method further comprising combining the first and second mixtures to make a single mixture (cassettes were individually ligated into pGEM-T plasmids, column 24, lines 44-50) and differentially amplifying the first mixture and the second mixture in a PCR reaction by controlling amounts of the first primer set and the second primer set in the single mixture (primer amounts for the two primer sets were both used at 1.2 mM, column 31, lines 47-48, which generated different yields of exon 10 and 11 products, column 24, lines 12-25).

With regard to claim 74, Gordon teaches a method further comprising adding normal human nucleic acid to the single mixture to obtain heterozygous pairs, wherein each heterozygous pair includes a normal segment of human nucleic acid and a mutated copy of the normal segment of human nucleic acid (mixture of DNA control construct can contain fragments that comprise wild-type sequence of interest and as many mutations and variations as desired, column 20, lines 48-51 and column 24, lines 26-42; mutations were added by site directed mutagenesis, column 27, lines 19-22).

4. Claims 71, 72 and 74 are rejected under 35 U.S.C. 102(b) as being anticipated by Chenchik et al. (U.S. Patent No. 5,759,822).

With regard to claim 71, Chenchik teaches a method, comprising:

designing multiple reference nucleic acids (such as a cDNA library cloned into a vector, column 12, line 66 to column 13, line 2), wherein each reference nucleic acid

comprises an arrangement of bases emulating a clinically relevant site of a human nucleic acid *in vivo* (fragments may contain sequences used for mapping chromosome aberrations, column 13, lines 2-8) exclusive of clinically irrelevant human nucleic acid adjacent to the clinically relevant site (fragments corresponding to cDNA can be prepared free of the poly A-minus fractions or other genomic impurities, column 24, lines 8-12);

synthesizing, base by base for each reference nucleic acid, a first mixture of various of the reference nucleic acids, wherein each of the various reference nucleic acids in the first mixture includes one or more tags allowing PCR amplification of the first mixture via a primer set specific to the tags of the first mixture (Figure 3, top, two mixtures using same primer sets and adaptors, resulting in two populations of amplified products, Figure 3, bottom); and

synthesizing, base by base for each reference nucleic acid, a second mixture of various of the reference nucleic acids, wherein each of the various reference nucleic acids in the second mixture includes one or more tags allowing PCR amplification of the second mixture via a second primer set specific to the tags of the second mixture (Figure 3, top, two mixtures using same primer sets and adaptors, resulting in two populations of amplified products, Figure 3, bottom).

With regard to claim 72, Chenchik teaches a method, further comprising combining the first and second mixtures to make a single mixture and differentially amplifying the first mixture and the second mixture in a PCR reaction by controlling amounts of the first primer set and second primer set in the single mixture (amounts of

primers are kept at equal levels, but prevented from binding to pan structures, thus leading to differential amplification of the mixtures, Figure 3 and column 14, lines 5-20).

With regard to claim 74, Chenchik teaches a method, further comprising adding normal human nucleic acid to the single mixture to obtain heterozygous pairs, wherein each heterozygous pair includes a normal segment of human nucleic acid and a mutated copy of the normal segment of human nucleic acid (normal genomic sequences analyzed along with mutant sequences for chromosome mapping, column 12, line 66 to column 13, line 8 and Example 4 for example of human nucleic acid, skeletal muscle, column 24, lines 8-25).

Claim Rejections - 35 USC § 103

5. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

6. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

7. Claims 1, 2, 4, 5, 8, 9, 11, 16, 21-23 and 75-80 are rejected under 35 U.S.C. 103(a) as being unpatentable over Gordon et al. (U.S. Patent No. 6,607,911) in view of Strizhov et al. (U.S. Patent No. 6,110,668).

With regard to claim 1, Gordon teaches a method of creating a clinical reference solution that emulates clinically relevant sites on genes responsible for human genetic conditions (such as multiple and distinct mutations in a gene, column 16, lines 29-32), wherein the clinical reference solution is substantially free of clinically irrelevant nucleic acid (fragments of control DNA construct used as reference standard may contain, for example, only exons and their intronic borders from human cystic fibrosis transmembrane conductance regulator (CFTR) gene, each with associated mutant, column 16, lines 26-32), comprising:

for each clinically relevant site, designing an arrangement of bases to emulate the clinically relevant site as isolated from clinically irrelevant nucleic acid that occurs adjacent to the corresponding clinically relevant site *in vivo* (fragments comprise exons of gene of interest, column 18, lines 38-40), wherein the arrangement of bases also includes one or more primer targets for differentially amplifying the clinically relevant site (one or more primer sites for PCR amplification were added to cassettes that also include unique restriction sites, column 23, lines 52-59);

for each clinically relevant site, synthesizing, base by base, from end to end, an artificial version of each arrangement of bases that emulates the clinically relevant site and forms the primer targets associated with the clinically relevant site (fragments containing cassettes were amplified using unique priming sites, column 23, line 60 to

column 24, line 3; fragments can also be made chemically or by other means, column 22, lines 30-37); and

mixing each artificial version of a clinically relevant site into a single solution (cassettes were individually ligated into pGEM-T plasmids, column 24, lines 44-50).

With regard to claim 2, Gordon teaches a method wherein each clinically relevant site comprises a mutation of a normal human nucleic acid sequence (as measured in a Clinical Laboratory, column 6, lines 50-62), each mutation representing a human genetic condition (such as deltaF508 and deltaI507 in exons 10 and 11, respectively, in human CFTR gene, column 3, lines 12-27 and column 16, lines 29-32).

With regard to claim 4, Gordon teaches a method wherein:

the synthesizing one or more primer targets includes a first sequence of nucleotides attached base-by-base to a first end of the arrangements of bases, wherein the first sequence is complementary to a nucleotide sequence of a first primer of a primer set (BssH II restriction site was incorporated on 5' end of exon 10 used in making DNA control construct, and contained priming site for amplification, column 23, line 52 to column 24, line 3), and

the synthesizing one or more primer targets includes a second sequence of nucleotides attached base-by-base to a second end of the arrangements of bases, wherein the second sequence is identical to a nucleotide sequence of a second primer of a primer set (Csp45 I restriction site was incorporated on 3' end of exon 10 used in making DNA control construct, and contained priming site for amplification, column 23, line 52 to column 24, line 3).

With regard to claim 5, Gordon teaches a method wherein the synthesizing comprises synthesizing, base-by-base, two complementary nucleic acid strands (strands are synthesized by PCR, column 23, line 60 to column 24, line 3), wherein:

a first strand includes one of the clinically relevant sites and a nucleic acid tag complementary to a first primer of a primer set (first strand of DNA control construct contains exon 10 or 11 and a unique mutation, and also has priming site on 5' end, column 23, lines 52-59); and

a second strand is complementary to the first strand and to a nucleic acid tag complementary to a second primer of the primer set (second strand of DNA control construct contains exon 10 or 11 and a unique mutation, and also has priming site on 3' end, column 23, lines 52-59).

With regard to claim 8, Gordon teaches a method wherein:

each clinically relevant site has an associated primer set (primer set for exon 10, for examples, uses primers that bind in unique BssH II and Csp45 I restriction sites, column 23, lines 52-65), and wherein:

the reference solution is tuned for a specific battery of clinical tests by differentially amplifying the different clinically relevant sites to different concentrations in the reference solution (different concentrations of serial dilutions of plasmid containing DNA control construct were amplified using biotin-labeled primers for a set amount of cycles and added to microplate containing samples for hybridization and quantification, column 31, line 28 to column 32, line 28).

With regard to claim 9, Gordon teaches a method wherein different groups of the clinically relevant sites in the reference solution have associated primer sets such that each different group of clinically relevant sites is amplified independently (unique primer sets can be used in a construct containing cassettes for exons 10 and 11 to amplify each independently, column 23, line 60 to column 24, line 25).

With regard to claim 11, Gordon teaches a method wherein independently amplifying each of the groups of clinically relevant sites includes controlling a physical characteristic of the reference solution to favor an amplification capability of one primer set over an amplification capability another primer set (exon 11 cassette PCR reactions amplified the target more efficiently using shorter extension times, than the reactions of exon 10 cassette, which required longer extension times while still generating lower product yields, column 24, lines 4-25) .

With regard to claim 16, Gordon teaches a method further comprising adding normal human nucleic acid to the base by base synthesized clinically relevant sites in order to achieve a mixture of the nucleic acids in the reference solution representing at least a segment of homologous heterozygous alleles (mixture of DNA control construct can contain fragments that comprise wild-type sequence of interest and as many mutations and variations as desired, column 20, lines 48-51 and column 24, lines 26-42; mutations were added by site directed mutagenesis, column 27, lines 19-22).

With regard to claim 21, Gordon teaches a method further comprising joining two parts of one of the arrangements of bases together using a ligation extension to perform the synthesizing of a large arrangement of bases (two or more fragments may be

ligated together, each containing unique sites at their termini and wherein each site overlaps the adjacent or flanking site, in order to produce larger construct containing multiple cassettes, column 17, lines 1-11).

With regard to claim 22, Gordon teaches a method further comprising using a bridge nucleic acid to join multiple parts of the arrangement of bases (ends of fragments can be modified to form sticky ends to facilitate ligation to each other, column 18, lines 2-4).

With regard to claim 23, Gordon teaches a method further comprising using an overlap extension to join multiple parts of the arrangement of bases (exon 10 and 11 cassettes were joined together after digestion by ligation using their common restriction sites and A overhangs, column 24, lines 47-50 and column 26, lines 19-30).

With regard to claims 75-77, Gordon teaches a method further comprising differentially amplifying each different strand in the solution to a respective clinically relevant concentration, wherein the amplifying increases the number of each strand exponentially and wherein each strand creates its own complementary single strand during the amplifying (unique primer sets can be used in a construct containing cassettes for exons 10 and 11 to amplify each independently wherein complementary strands for the strand at each site are synthesized during exponential amplification, column 23, line 60 to column 24, line 25).

With regard to claims 78-80, Gordon teaches a nucleic reference fragment that mimics a genomic reference sample wherein the nucleic acid reference fragment is capable of being differentially amplified to a concentration suitable for use as a clinical

reference and wherein the reference fragment creates its own complementary single strand during the amplifying (construct containing cassettes for exons 10 and 11 can be differentially amplified using separate primer sets and unique reaction conditions to create double-stranded product containing two complementary strands, column 23, line 60 to column 24, line 25; mutations to add clinically relevant mutations to mimic a genomic reference sample can be added to either fragment of the construct by site-directed mutagenesis, column 27, line 58 to column 28, line 15).

Gordon does not teach a method of creating a clinical reference solution wherein for each clinically relevant site, a single strand of bases is synthesized base-by-base, from end to end that forms the primer targets associated with the clinically relevant site.

Strizhov teaches a method of gene synthesis wherein chemically-synthesized oligonucleotides are ligated together using a partially homologous template to produce a new single-stranded synthetic DNA product with primer targets at each end so that the single-stranded product can be amplified by PCR (column 2, lines 52-63, column 5, line 63 to column 6, line 8 and Figure 1). The end-primer sites form restriction cleavage sites upon amplification for use in cloning of the synthetic double-stranded fragments (column 2, lines 63-65 and column 6, lines 8-40).

Strizhov does not teach a method of creating a clinical reference solution wherein the clinical reference solution is substantially free of clinically irrelevant nucleic acid comprising an arrangement of bases to emulate the clinically relevant site as isolated from clinically irrelevant nucleic acid that occurs adjacent to the corresponding clinically relevant site *in vivo*.

It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to combine the methods of Gordon for producing reference control DNA constructs and the methods of Strizhov for producing chemically-synthesized single-stranded gene products containing end-primers since the single-stranded products can be readily amplified and used in the methods of Gordon for creating double-stranded cassettes containing fragments that correspond to mixtures of reference control DNAs. Thus, an ordinary practitioner would have been motivated to use the methods of Strizhov to produce chemically-synthesized single-stranded products containing primer binding sites at each end since these products can be amplified by primers unique to the single-stranded product, and the double-stranded PCR products then cloned or ligated into a vector to produce a cassette clone following cleavage by restriction endonucleases that recognize cleavage sites designed in the primer sites (Strizhov, column 6, lines 8-11) wherein each cassette can be amplified independently with unique primer sets to produce a mixture of reference DNAs (Gordon, column 23, line 60 to column 24, line 25). Alternatively, the products representing different reference nucleic acids could be combined directly after amplification to provide a mixture of reference nucleic acids, each strand containing two primer sites. The methods of Strizhov utilize a combination of enzymatic and chemical synthesis of DNA to significantly reduce the cost, time and number of steps required for making artificial gene constructs containing unique priming sites (Strizhov, column 2, lines 45-51) that could be used as clinical reference standards in the methods of Gordon. In fact

Gordon suggests alternate methods for construction of reference fragments including the use of chemical synthesis (Gordon, column 22, lines 30-37).

Response to Arguments

8. Applicant's arguments filed May 24, 2007 have been fully considered but they are not persuasive.

Applicant argues that the 35 USC § 102(b) rejection of claims 1, 2, 4, 5, 7-9, 11, 16, 21-23, and 71-74 as being anticipated by Chenchik et al. (U.S. Patent No. 5,759,822) should be withdrawn since the reference no longer anticipates the claims as amended. In particular, Applicant argues that Chenchik does not disclose synthesizing a clinically relevant reference nucleic acid as a single strand of bases in a base-by-base manner that also contains the primer targets for amplification. The Examiner agrees that the Chenchik reference no longer meets the limitations of claims 1, 2, 4, 5, 7-9, 11, 16, 21-23 as amended since Chenchik does not teach synthesis of a single strand of bases containing both primer sites, and therefore the 102(b) rejection of these claims is withdrawn. However, claims 71, 72 and 74 are still anticipated by Chenchik since these claims do not contain the new limitations.

Applicant then argues that the 35 USC § 102(b) rejection of claims 1, 2, 4, 5, 7-9, 11, 16, 21-23, and 71-74 as being anticipated by Gordon et al. (U.S. Patent No. 6,607,911) should be withdrawn since the reference no longer anticipates the claims as amended. In particular, Applicant argues that Gordon does not disclose synthesizing a clinically relevant reference nucleic acid as a single strand of bases in a base-by-base manner that also contains the primer targets for amplification. The Examiner agrees

that the Gordon reference no longer meets the limitations of claims 1, 2, 4, 5, 7-9, 11, 16, 21-23 as amended since Gordon does not teach synthesis of a single strand of bases containing both primer sites, and therefore the 102(b) rejection of these claims is withdrawn. However, claims 71, 72 and 74 are still anticipated by Gordon since these claims do not contain the new limitations.

Upon further searching, another reference was found that teaches production of single-stranded gene constructs containing primer sites at each end that can be used in the methods of Gordon for producing cassettes of reference DNAs (Strizhov et al. (U.S. Patent No. 6,110,668). Therefore, claims 1, 2, 4, 5, 7-9, 11, 16, 21-23 and 75-80 are now rejected under 35 U.S.C. 103(a) as being anticipated by Gordon in view of Strizhov. The dependent claims are not separately argued over Gordon. With regard to claim 1, Strizhov makes up for the deficiency of Gordon by teaching methods for production of a single-stranded product using chemically synthesized oligonucleotides which are ligated together using a template. The single-stranded product contains primer binding sites at each end and the template is removed after amplification of the single-stranded product since only this product contains the binding sites for the amplification primers (Strizhov, column 6, lines 4-8). The product can be cloned into a vector using restriction sites designed into the primer sites (Strizhov, column 6, lines 8-11) to produce a cassette clone wherein each cassette can be amplified independently with unique primer sets to produce a mixture of reference DNAs (Gordon, column 23, line 60 to column 24, line 25).

Applicant also argues that the method of Gordon is beyond the scope of the instant application since multiple primer sets are needed to amplify each cassette instead of a common set. There is no limitation in the claims requiring a common primer set for amplification of different reference nucleic acids. However, one of ordinary skill in the art would recognize that different single-stranded products generated by the methods of Strizhov could easily be designed to comprise common primer binding sites at each end to allow simultaneous amplification with a single primer pair after cloning into the cassette clone. As an alternative to the cloning step, the single-stranded products taught by Strizhov representing different reference nucleic acids could be combined directly after amplification to provide a mixture of reference nucleic acids, each strand containing two primer sites, which can be either unique or common binding sites. Finally, Applicant argues that the artificial primer sites introduced for generating the cassettes are not used in downstream testing like the reference nucleic acids of the instant application. The cassette reference solution is in fact amplified by PCR during testing of samples for CFTR mutations after serial dilution of clone stocks (Gordon, column 31, lines 7-42) or using biotin-labeled primers for a colorometric assay (Gordon, column 31, lines 43-57).

Conclusion

9. Claims 1, 2, 4, 5, 8, 9, 11, 16, 21-23, 71, 72 and 74-80 are rejected. No claims are allowable.

Correspondence

10. Any inquiry concerning this communication or earlier communications from the examiner should be directed to David C. Thomas whose telephone number is 571-272-3320 and whose fax number is 571-273-3320. The examiner can normally be reached on 5 days, 9-5:30.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on 571-272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

David C. Thomas 9/25/07
David C. Thomas
Patent Examiner
Art Unit 1637

JEFFREY FREDMAN
PRIMARY EXAMINER
9/25/07